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TRANSPORTER PROTEIN SPLICE VARIANTS
AND MODEL FOR IMMUNE DIVERSITY

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Field of the Invention

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The present invention relates to the discovery of nonallelic TAP polymorphs and to a new model of immune diversity based by this discovery. More specifically, the invention relates to TAP splice variants, which lead to the formation of a previously unknown class of MHC class I antigen complexes being presented to the immune system on MHC class I-presenting cells. A new layer of diversity is thus discovered for the immune system, in addition to the allelic variation in MHC class I molecules and the genetic rearrangements leading to diversity in the T cell receptor repertoire.

Background of the Invention

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Class II and class I proteins encoded by genes of the Major Histocompatibility Complex (MHC) on chromosome 6 in humans play an essential role in regulating the immune system. MHC class II molecules, which are expressed in antigen-presenting cells such as macrophages, B cells, monocytes and some epithelial cells, form complexes with antigen peptides ("MHC class II antigen complexes") that are displayed on the surface of antigen-presenting cells for recognition by CD4+ T lymphocytes (helper T cells). Helper T cell recognition results in release of lymphokines and T-dependent activation of B cells, which, in turn, lead to activation of macrophages and release of

antibodies from B cells, leading to the killing or elimination of invading microorganisms. MHC class I molecules, which are expressed in virtually all nucleated cells, form complexes with antigen peptides ("MHC class I antigen complexes") that are displayed on the cell surface for recognition by CD8+ cytotoxic T lymphocytes (CTLs). Presentation of an endogenous or "self" peptide by the MHC class I antigen complex is protective, the CTLs that would otherwise recognize the surface complex and attack the presenting cell (i.e., autoreactive CTLs) having been eliminated (deleted) from the immune system repertoire; and presentation of an exogenous (foreign or "non-self") peptide (or a mutated endogenous peptide) by the MHC class I antigen complex elicits CTL attack and cytolytic destruction of the infected or diseased cell.

The peptides that complex with MHC molecules are approximately eight to twenty-four amino acids in length. In the case of class II antigen complexes, the peptides are derived from partial proteolysis and processing of extracellular antigenic proteins incorporated by the cell through phagocytosis or pinocytosis or possibly surface processing. Thus, the immune recognition events mediated by MHC class II antigen complexes are a primary defense to invading microorganisms (e.g., bacteria, parasites) or foreign substances (e.g., haptens, transplant tissues) introduced to the cells of the immune system via the circulatory or lymph systems. In the case of class I antigen complexes, the antigen peptides are derived from intracellular processing of proteins. Thus, MHC class I antigen complexes either mark the cell as a normal endogenous cell, which elicits no immune response, or mark the cell as an infected cell (e.g., as in the case of a virus-infected cell exhibiting intracellularly processed viral (i.e., foreign) peptide in the surface MHC class I complex) or a transformed cell (e.g., such as a malignant cell), which marks the cell for attack by CTLs.

Proper intracellular processing of antigen peptides for MHC class I complexing and presentation involves several steps. One of these steps is transport of the peptides from the cytosol into the endoplasmic reticulum (ER), where coupling of the antigen peptide with the MHC class I molecule takes place. The MHC class I antigen complex migrates to the cell surface for presentation and possible recognition by T cells. Unsuccessful transport of peptides into the ER, or other abnormalities leading to faulty class I antigen complex formation or presentation, can lead to a failure in recognizing autologous cells as "self". For example, defects in genes coding for transporter proteins have been discovered to be an underlying cause of several autoimmune diseases (Faustman et al., *Science*, 254:1756-1761 (1991); U.S. Patent No. 5,538,854).

Transporter associated with Antigen Processing, or TAP, proteins transport peptide fragments of eight or more amino acids from the cytosol of a cell into the lumen of the ER, where the peptides are bound by MHC class I proteins to form an antigen complex, which ultimately is displayed on the surface of the cell (see, e.g., Powis et al., *Immunogenetics*, 37:373-380 (1990)).

The TAP protein is a heterodimer of the products of the *TAP1* and *TAP2* genes, which are also located in the MHC region of the genome. Each subunit of the TAP1/TAP2 heterodimer forms an ATP-binding domain and a domain that criss-crosses the membrane six to eight times, and both subunits are required to form a peptide binding site and to translocate peptide into the ER (Androlewicz et al., Proc. Natl. Acad. Sci. USA, 91(26): 12716-12720 (1994); Hill et al., Proc. Natl. Acad. Sci. USA, 92: 341-343 (1995)).

The role of TAP in mediating the supply of antigen peptides transported into the ER and ultimately displayed by MHC class I molecules has caused close scrutiny of the range of peptides capable of translocation by TAP, to determine whether TAP is a further restrictive factor in immune diversity. (See, Hill et al., *ibid.*; Howard, Proc. Natl. Acad. Sci. USA, 90: 3777-3779 (1993).) Whereas gene rearrangement during ontogeny of T cells generates an enormous variety of T cell receptor specificities, making the recognition capability of the immune system very diverse, there has not been discovered any corresponding mechanism for diversifying the presentation capability of an individual's immune system. Although small variations in MHC allotypes result in different repertoires of antigen peptides being complexed and presented by MHC molecules, lending diversity to antigen presentation across a species, an individual's MHC haplotypes restrict the range of antigens that can be effectively displayed. The specificity of the TAP transport mechanism also shapes the repertoire of antigen complexes presented to the immune system, in that only peptides capable of translocation by TAP are made available for complexing in the ER with MHC class I. (See, Howard, *ibid.*)

The peptide specificity of TAP proteins has been studied in three species thus far: human, mouse and rat. In the rat, it was shown that different alleles of the *TAP2* gene gave rise to functional polymorphism, i.e., the different alleles transported sets of peptides that differed in C-terminal residues. (Powis et al., Immunity, 4(2):159-165 (1996); Powis et al., Nature, 357:211-215 (1992).) In the human and mouse, however, investigation of several polymorphs of TAP1 and TAP2 did not reveal any alteration in the spectrum of peptides transported, and it has been generally concluded that although in mice and humans the TAP1 and TAP2 proteins are genetically polymorphic, they are functionally monomorphic, the sequence alterations of the allotypes causing no shift in the types of peptides translocated by TAP. (Schumacher et al., Proc. Natl. Acad. Sci. USA, 91(26):13004-13008 (1994); Obst et al., Eur. J. Immunol., 25: 2170-2176 (1995); Daniel et al., J. Immunol., 159: 2350-2357 (1997).)

It has now been unexpectedly discovered that the human *TAP1* and *TAP2* genes produce several splice variants that differ structurally and functionally from the known TAP1 and TAP2

proteins, and functional TAP1 and TAP2 splice variant gene products, designated TAP1iso³ and TAP2iso, have been characterized and their full coding sequences isolated.

The TAP heterodimer including the TAP2iso splice variant, surprisingly, preferentially translocates a different set of peptides than the TAP heterodimer including TAP2. These discoveries have led to a revision described herein of the model of peptide transport into the lumen of the ER for MHC class I complexing; and a new level of diversity in the presentation of antigen complexes, akin in some respects to the diversity of T cell receptors in the recognition of such complexes, has been exposed for the first time.

10 Summary of the Invention

The present invention provides novel TAP1 and TAP2 splice variants and novel functional TAP heterodimers (i.e., a TAP1 subunit complexed with a TAP2 subunit) including at least one splice variant of TAP1 or TAP2. The TAP splice variants alter peptide transport to the ER in comparison with the previously known TAP complex. "Altered peptide transport" includes preferential transport of a specific repertoire of peptides that differs (e.g., in length or amino acid content or structure) from that transported by the previously known TAP protein (TAP1/TAP2 heterodimer), and/or a change in the rate of peptide transport into the ER as compared to known TAP. TAP splice variants according to the invention preferably measurably affect the repertoire of peptides displayed as MHC class I antigen complexes on the surface of antigen presenting cells or affect the cell surface density of particular MHC class I antigen complexes.

A specific embodiment of the present invention is designated TAP2iso (SEQ ID NO: 2). TAP2iso differs from the previously known TAP2 protein (see SEQ ID NO: 15) by a deletion of a C-terminal sequence corresponding to exon 11 of the human gene encoding TAP2 and the insertion in-frame with exon 10 of newly discovered exon 12 (SEQ ID NO: 5). Isolated nucleic acids encoding TAP2iso are also disclosed (see, e.g., TAP2iso cDNA, SEQ ID NO: 4). Another specific embodiment is designated TAP1iso³ (SEQ ID NO: 25), which differs from the previously known TAP1 (see SEQ ID NO: 19) by deletion of the C-terminal sequence corresponding to exons 9-11 and the transcription of additional sequence 3' of exon 8, leading to the addition of several amino acids (see item 8a in Fig. 11). Further embodiments of this invention relate to additional TAP1 and TAP2 splice variants that have been detected by RT-PCR studies. Specific additional splice variants thus far detected are designated TAP1iso, TAP1iso² and TAP2iso².

The TAP1 and TAP2 splice variants of the present invention are unique arrangements and/or combinations of TAP1 and TAP2 exons. The TAP 1 and 2 splice variants are functional in that each splice variant complexes with at least one corresponding TAP subunit to form a TAP1-type

subunit/TAP2-type subunit complex (a TAP heterodimer), which preferably is capable of translocating peptides.

The present invention relates also to novel TAP1 and TAP2 exons, by which the splice variants differ from known TAP1 and TAP2 coding sequences (see SEQ ID NOs: 18 and 17, respectively), and to the peptides encoded by those exons, which are useful, e.g., as immunogens for production of antibodies that can selectively recognize the splice variant proteins from mixed populations of TAP gene products.

The discovery of a genetic link to the repertoire of antigen peptides that are transported intracellularly to form MHC class I antigen complexes raises the possibility that variation in the complement of TAP1 or TAP2 gene products in humans will be associated with autoimmune disease. Thus, a deletion or a mutation in a splice variant exon may result in a failure to present certain endogenous peptides, leading in turn to autoreactive CTL attack of self tissues. Alteration of the ratio of co-expressed TAP subunit variants may also be associated with disease. And defective production of a particular variant of the TAP genes may provide an opening in the immune presentation-and-recognition system allowing malignant cells or virally infected cells to escape detection and to survive where they would be attacked and eliminated in another (normal) individual. This invention provides methods for detection and treatment of such disorders associated with abnormalities in TAP splice variant expression.

This invention also provides new methods for designing vaccines to broaden the immune response of individuals that may be unresponsive to a standard vaccine due to inadequate processing of particular viral antigens, for instance due to their expression of MHC class I alleles that do not efficiently display antigen peptides from available vaccine preparations. To broaden an individual's immune response to a particular virus, cells from the individual, e.g., lymphocytes (preferably macrophages, B cells or dendritic cells) are withdrawn and transfected with a gene encoding a TAP isoform that is not expressed or poorly expressed in that individual, transfectants are recovered that express the inserted TAP isoform DNA, and then the cells are returned to the individual. The TAP isoform gene may be non-specific, provided simply to broaden the range of peptides processed by the cells, or specific for providing translocation of particular viral antigen peptides. The transfected cells, expressing an additional TAP isoform will supplement the repertoire of antigen peptides processed and displayed to the immune system as MHC class I antigen complexes, leading to recognition by CD8-positive (CD8+) T cells and the development of T cell memory for those antigen complexes. Thereafter, the vaccinated individual will display a secondary antigen response to challenge from the virus. Similar methods will be useful for improving immune response against infectious diseases or tumor cells that escape an individual's normal antigen processing capability.

Brief Description of the Drawings

Fig. 1 depicts the organization of genomic human *TAP2* genes and the structures of *TAP2* and *TAP2iso* cDNAs. The open boxes represent exons 1 to 10, which, sharing the same 5' untranslated region (5'-UT), are present in both *TAP2* and *TAP2iso* cDNAs. The alternatively spliced exons 11 and 12, together with their corresponding 3' untranslated regions (3'-UT), are hatched.

Fig. 2 illustrates the sequence analysis of the exon junctions of *TAP2* (clone 0121) and *TAP2iso* (clone 01023) cDNAs isolated from the same human spleen cDNA library. Two full-length cDNA clones, 0121 and 0123, represent two different forms of human *TAP2* cDNA. Clone 0121 corresponds to the previously known *TAP2* isoform, in which exon 10 is spliced at transcription to exon 11. Clone 0123 represents the newly discovered *TAP2iso* cDNA, in which exon 10 is spliced to exon 12.

Fig. 3 illustrates electrophoresis results of RT-PCR products showing co-expression of *TAP2* and *TAP2iso* mRNAs in various human cell lines, along with β_2 -microglobulin (β_2). Lanes: (0) DNA molecular size markers; (1) T1 cells (human lymphoblastoid B cell line); (2) T2 cells (human lymphoblastoid B cell line of T1 origin with a large homozygous deletion of the MHC class II gene region containing *TAP1* and *TAP2*); (3 and 4) fresh human peripheral blood lymphocytes from two different donors; (5 and 6) Epstein-Barr virus-immortalized B cell lines from two different donors; (7) MOLT-4 acute lymphoblastic leukemia cells; (8) THP-1 monocytic cells; (9) U-937 histocytic lymphoma cells; (10) HeLa epithelioid carcinoma cells; (11) PACA pancreatic carcinoma cells.

Figs. 4A and 4B illustrate electrophoresis results showing the effect of *TAP2iso* together with *TAP1* on the maturation of MHC class I molecules in the ER of T2 cells transfected with *TAP1* and *TAP2iso* (Fig. 4A) as compared with untransfected T2 cells (Fig. 4B) incubated in the absence (-) or presence (+) of endoglycosidase H (endo H) at various time points. "r" and "s" indicate class I proteins resistant and sensitive to endo H, respectively. The increased rate of class I maturation in *TAP1/TAP2iso*-transfected cells is reflected by the difference in endo H sensitivity compared with untransfected cells.

Fig. 5 illustrates peptide selectivity of *TAP1/TAP2* and *TAP1/TAP2iso* heterodimers in permeabilized T2 transfectants. Three different glycosylated and radiolabeled (^{125}I) peptides, RRYQNSTEL (SEQ ID NO: 6), IYLGPFSPNVTL (SEQ ID NO: 7) and TVDNKTRYE (SEQ ID NO: 8) were recovered and measured. The data presented are means of three separate experiments employing ten different sets of transfectants. The amount of translocated peptide is shown as a percentage of the total amount of radiolabeled peptide introduced. The results demonstrate that

RRYQNSTEL was translocated with equal efficiency by TAP1/TAP2 or TAP1/TAP2iso heterodimers, but that IYLGPFSPNVTL was transported four times more efficiently by the TAP1/TAP2iso heterodimer compared to the TAP1/TAP2 transporter, and that TVDNKTRYE was transported more efficiently in the TAP1/TAP2 transfectant.

Figs. 6A, 6B, 6C, 6D and 6E illustrate competitive transport efficiency in transfected T2 cells. The peptide RRYQNSTEL (SEQ ID NO: 6) is analyzed for transport efficiency in competition with itself (Fig. 6A), in competition with IYLGPFSPNVTL (SEQ ID NO: 7) (Fig. 6B), in competition with TVDNKTRYE (SEQ ID NO: 8) (Fig. 6C), in competition with SYSMEHGRWGKPVGKKRRPVKVYP (SEQ ID NO: 9) (Fig. 6D), and in competition with RGFFYTPKA (SEQ ID NO: 10).

Fig. 7 compares relative fifty percent inhibitory concentrations (IC 50) of the test peptides (RRYQNSTEL, IYLGPFSPNVTL, and TVDNKTRYE) in T1 cells (which naturally co-express both TAP2 and TAP2iso) and T2 transfectants expressing either TAP1/TAP2 or TAP1/TAP2iso. The T1 cells show transportation of all the test peptides with equal efficiency, whereas the transfectants exhibit preferential transport of one of the three test peptides in comparison to RRYQNSTEL.

Fig. 8 illustrates electrophoresis results showing co-transcription of TAP1iso and TAP1iso² mRNAs in EBV-stabilized cells from various human subjects. Lanes: (1) DNA molecular size markers; (2) genomic DNA from a first individual (Control #1); (3) nuclear RNA from Control #1; (4) cytoplasmic mRNA from Control #1; (5) total RNA from Control #1, without DNAase digestion; (6) total RNA from Control #1, with DNAase digestion; (7) cytoplasmic mRNA from a second individual (Control #2), with DNAase digestion; (8) cytoplasmic mRNA from a third individual (Control #3), with DNAase digestion; (9) cytoplasmic mRNA from a fourth individual (Control #4), with DNAase digestion; (10) cytoplasmic mRNA from a diabetic patient, with DNAase digestion.

Figs. 9A and 9B show the comparative sequences of the PCR products indicating the presence of splice variants TAP1iso and TAP1iso² (Fig. 9A) and a schematic diagram of the genomic DNA including TAP1 exons 9-11, with diagrams of the TAP1iso and TAP1iso² messages, both including exons 9 and 10 but two different segments of intron 10 (Fig. 9B).

Fig. 10 illustrates electrophoresis results showing co-transcription in several individuals of a fully spliced TAP2 and a variant in some individuals presumably retaining part of intron 10. The second product indicates a further TAP2 splice variant, designated TAP2iso². All lanes show PCR products of cDNA derived from cytoplasmic mRNA from fresh peripheral blood lymphocytes (PBLs) from several normal and one hypothyroid individual. Lanes: (1) Control (normal) individual 1; (2) Control individual 2; (3) hypothyroid patient; (4) Control individual 3; (5) Control individual

4; (6) Control individual 5; (7) Control individual 6; (9) Control individual 7; (10) Control individual 8; (11) control genomic DNA sample.

Fig. 11 depicts the organization of genomic human *TAP1* genes and the structures of *TAP1* and *TAP1iso*³ cDNAs. The open boxes represent exons 1 to 8, which, sharing the same 5' untranslated region (5'-UT), are present in both *TAP1* and *TAP1iso*³ cDNAs. The exons 9, 10 and 11, together with their corresponding 3' untranslated regions (3'-UT), are hatched. These exons are spliced-in in the expression of *TAP1* but are spliced-out in the discovered *TAP1iso*³, which is composed of the exons 1 through 8 and additional amino acids encoded by a portion of intron 8 (marked 8a) and its corresponding 3' untranslated region (3'-UT), which are reverse-hatched.

Definitions

The following illustrative explanations are provided to facilitate understanding of certain terms and phrases frequently used and of particular significance herein. Throughout this specification, TAP proteins will be referred to using unitalicized type (e.g., "TAP2" and "TAP2iso"), and the corresponding genetic materials or polynucleotides coding for such TAP proteins will be referred to using italics (e.g., "*TAP2*" and "*TAP2iso*" genes)

The term "exon polypeptide", as used herein, refers to the peptide corresponding to the portion of a protein encoded by the DNA of a particular exon. Thus, the exon 12 polypeptide of the present invention, Lys-Thr-Leu-Trp-Lys-Phe-Met-Ile-Phe (SEQ ID NO: 1), is the polypeptide comprising the amino acids encoded by exon 12 of the *TAP2iso* coding sequence.

The term "splice variant", as used herein, refers to a gene product that is homologous to a known gene product and is generated by alternative RNA splicing during transcription. The splice variant will be partially identical in sequence to the known homologous gene product, corresponding to the extent of identity of exon use, comparing the mRNA transcripts (or cDNA), between the known product and the splice variant. Thus, the TAP2 splice variant described herein that is designated TAP2iso (SEQ ID NO: 2), is homologous to the previously known TAP2 protein (SEQ ID NO: 15), and the two gene products have common N-terminal amino acid sequences corresponding to the amino acids encoded by exons 1-10 of the *TAP2* gene, and the amino acid sequences differ C-terminally to the exon 10 polypeptide, with TAP2 terminating with the exon 11 polypeptide (SEQ ID NO: 16) but TAP2iso terminating instead with the exon 12 polypeptide (SEQ ID NO: 1). By virtue of the partial identity and partial divergence of their amino acid sequences, the splice variant and the known homologues will have some functionality in common but will differ in other functions. For example, as shown herein, TAP2 and TAP2iso both (in a TAP complex with a TAP1 subunit) perform the function of translocating peptides into the lumen of the ER for MHC

class I antigen complex assembly, but TAP2iso transports a repertoire of peptides that differs from that of TAP2, or transports the same peptides at a rate or with an efficiency that differs from TAP2.

The splice variants described herein form heterodimers with corresponding TAP subunits, and the functional TAP proteins formed by association of a splice variant with a known TAP subunit or by association of two splice variants are also new. TAP heterodimers including at least one subunit that is a splice variant will be referred to herein as "TAPiso" proteins, which will be understood to be comprised of one TAP1-type subunit and one TAP2-type subunit, where one or both of the subunits are splice variants of the known TAP1 and TAP2 subunits (e.g., TAP1iso/TAP2, TAP1/TAP2iso, TAP1/TAP2iso² and TAP1iso/TAP2iso heterodimers, and the like, are specific examples of "TAPiso proteins").

The term "homologous", as used herein, refers to the degree of sequence similarity between two polymers (i.e., polypeptide molecules or nucleic acid molecules). When the same nucleotide or amino acid residue occupies a sequence position in the two polymers under comparison, then the polymers are homologous at that position. The percent homology between two polymers is the mathematical relationship of the number of homologous positions shared by the two polymers divided by the total number of positions compared, the product multiplied by 100. For example, if the amino acid residues at 60 of 100 amino acid positions in two polypeptide sequences match or are homologous then the two sequences are 60% homologous. The homology percentage figures referred to herein reflect the maximal homology possible between the two polymers, i.e., the percent homology when the two polymers are so aligned as to have the greatest number of matched (homologous) positions.

The present invention further relates to isolated nucleic acids (or "polynucleotides") that hybridize to the TAP splice variant nucleic acid sequences described herein if there is sufficient homology between the TAP coding sequence and the complement of the homologous coding sequence to hybridize to each other under conditions equivalent to, e.g., about 20° to 27°C below T_m and 1M NaCl. The present invention particularly contemplates nucleic acid sequences that hybridize under stringent conditions to the TAP splice variant coding sequences described herein and complementary sequences thereof. For the purposes of this invention, the term "stringent conditions" means hybridization will occur only if there is at least 95% and preferably at least 97% identity between the nucleic acid sequences. Thus, the present invention particularly contemplates polynucleotides encoding TAP splice variants having the particular nucleic acid sequences described herein, or polynucleotides that are at least 95% identical to such sequences, and polynucleotides having sequences that are complementary to the aforementioned polynucleotides. The polynucleotides of the present invention that hybridize to the complement of TAP splice variant

coding sequences described herein preferably encode polypeptides that retain substantially the same biological function or activity as the mature TAP splice variant polypeptides encoded by the splice variant sequences to which they hybridize.

The term "isolated" means that the material is removed from its original or native environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated by human intervention from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of the environment in which it is found in Nature. Similarly, as used herein, the term "substantially purified" is used in reference to a substance that has been separated or otherwise removed, through human intervention, from the immediate chemical environment in which it occurs in Nature. Substantially purified polypeptides or nucleic acids may be obtained or produced by any of a number of techniques and procedures generally known in the field.

The present invention incorporates by reference methods and techniques well known in the field of molecular and cellular biology. These techniques include, but are not limited to techniques described in the following publications:

Old, R.W. & S.B. Primrose, Principles of Gene Manipulation: An Introduction To Genetic Engineering (3d Ed. 1985) Blackwell Scientific Publications, Boston. Studies in Microbiology; V.2:409 pp. (ISBN 0-632-01318-4).

Miller, J.H. & M.P. Calos eds., Gene Transfer Vectors For Mammalian Cells (1987) Cold Spring Harbor Laboratory Press, NY. 169 pp. (ISBN 0-87969-198-0).

Mayer, R.J. & J.H. Walker eds., Immunochemical Methods In Cell and Molecular Biology (1987) Academic Press, London. 325 pp. (ISBN 0-12480-855-7).

Sambrook, J. et al. eds., Molecular Cloning: A Laboratory Manual (2d Ed. 1989) Cold Spring Harbor Laboratory Press, NY. Vols. 1-3. (ISBN 0-87969-309-6).

Winnacker, E.L., From Genes To Clones: Introduction To Gene Technology (1987) VCH Publishers, NY (translated by Horst Ibelgafts). 634 pp. (ISBN 0-89573-614-4).

Description of the Preferred Embodiments

The present invention relates to the discovery of previously unknown isoforms homologous to the known TAP protein subunits (TAP1 and TAP2, see SEQ ID NOs: 18 and 17 (coding sequences) and SEQ ID NOs: 19 and 15 (amino acid sequences)). The newly discovered isoforms are the result of alternate RNA splicing and are co-expressed with the known TAP1 and TAP2 gene products, providing a plurality of TAP heterodimers functioning to translocate antigen peptides from the cytoplasm into the endoplasmic reticulum for complexing with MHC class I molecules and formation of MHC class I antigen complexes. The splice variant isoforms have been found to form TAP heterodimers that transport a different repertoire of peptides or that transport similar peptides at different rates (i.e., with greater or lesser efficiency) than the known TAP1/TAP2 heterodimer; and the discovery of these alternate TAP transporter proteins exposes a genetic mechanism of diversification in the process of MHC class I antigen presentation. Co-expression of multiple TAP1 and TAP2 splice variants provides a diverse family of transporters capable of translocating a wider range of antigen peptides from the cytosol to the ER and increasing the repertoire of MHC class I antigen complexes presented to the immune system. It is through such diversification mechanisms that it is now demonstrated that the antigen processing and presentation mechanisms of the immune system are able to drive and select T cell response diversity on the recognition side of the immune system, which is based on the enormous diversity of the T cell receptor (TCR).

Specific embodiments of the invention include novel splice variants of TAP1 and TAP2 and nucleic acids that encode them. Specific splice variants described herein are designated TAP1iso, TAP1iso², TAP1iso³, TAP2iso and TAP2iso². The invention further encompasses novel TAP heterodimers ("TAPiso" heterodimers) incorporating the splice variants, exon polypeptides corresponding to previously unknown segments of the splice variants (i.e., corresponding to the exons or translated regions of genomic DNA by which the splice variants differ from known TAP1 or TAP2), vectors for cloning and expression of the splice variants or novel exon polypeptides, and recombinant host cells capable of expressing the splice variants, exon polypeptides or TAPiso heterodimers. The nucleotide sequence of *TAP2iso* and the deduced amino acid residue sequence of TAP2iso are shown in the Sequence Listing (SEQ ID NO: 4 and SEQ ID NO: 2, respectively).

The discoveries of the present invention also raise the possibility that a deletion or defect in expression of a particular TAP1 or 2 isoform, or that an abnormal expression level of one TAP1 or 2 isoform with respect to another, may cause the manifestation of autoimmune disease. For example, the ratios of TAP2 isoforms co-expressed by individuals was compared: Five patients diagnosed with Type I diabetes and five unaffected non-diabetic individuals were tested for levels of expression of TAP2 and TAP2iso. It was observed that, whereas in the non-diabetic individuals

expression levels were about the same, in 4 out of 5 of the diabetic patients, expression of TAP2iso predominated. This supports the use of the discoveries disclosed herein for diagnosis of TAP-associated conditions, in this case Type I diabetes, be measuring co-expression levels of the various TAP isoforms, for example the ratio of TAP2iso:TAP2. Methods for diagnosis and methods of treatment of such diseases associated with defective TAP isoform expression are in more detail below.

An isolated nucleic acid (polynucleotide) that encodes the mature TAP2iso polypeptide having the deduced amino acid sequence of SEQ ID NO: 2 was deposited under the Budapest Treaty with ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209 (US)) under accession no. 209640 on February 24, 1998.

The ATCC microorganism deposit referred to above will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for purposes of Patent Procedure. The deposit is provided as a convenience to those of skill in the art and is not to be construed as an indication or admission that such a deposit is required under 35 U.S.C. §112 or is necessary for a complete understanding of the invention. The sequence of the polynucleotides contained in the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, is incorporated herein by reference and is controlling in the event of any conflict with any description of sequences herein. A license may be required to make, use or sell the deposited material, and no such license is hereby granted.

Isolation of TAP Subunit Splice Variants

Nucleic acids coding on expression for TAP1 or TAP2 splice variants according to this invention may be isolated by screening a cDNA library, such as a human splenocyte cDNA library. cDNA libraries may be screened using an oligonucleotide probe complementary to an exon of *TAP1* or *TAP2* (or, also, a probe complementary to an intron portion suspected of being an exon in a splice variant). Construction of suitable cDNA libraries is well known in the art. Any portion of a *TAP1* or *TAP2* mRNA or cDNA may be used, however it is preferred that the probe be designed so as not to span exons and to include coding sequences that are thought to be used in all isoforms. Thus far, variation in the *TAP1* and *TAP2* coding sequences has been discovered at the 3' end of the sequences, and therefore it is preferred to screen using probes based on the first nine or ten exons of *TAP1* and *TAP2*. Probes based on all or part of exons 8, 9 or 10 of *TAP1* or *TAP2* are most preferred.

Additional TAP subunit splice variants may also be isolated using reverse transcription polymerase chain reaction (RT-PCR) techniques: Now that the existence of TAP splice variants has

been discovered and disclosed herein, additional coding sequences for splice variants can be discovered by analysis of PCR products from segments of total RNA and mRNA (see the examples, *infra*). Forward and reverse PCR primer pairs can be designed from genomic sequence information disclosed herein or obtained elsewhere. The RT-PCR experiments set forth herein were greatly assisted by genomic sequence information on human chromosome 6 (which includes the *TAP* genes) that was generously provided by Dr. John Trowsdale and colleagues at the Imperial Cancer Research Fund, London. Primer pairs can be selected to amplify any segment of the *TAP* loci or, in RT-PCR, any segment of cDNA derived from total RNA, however it is preferred to select primer pairs that are about 300-500 base pairs apart, so that disparate co-amplified products can be readily distinguished, e.g., by separation on an electrophoresis gel. It is preferred to employ overlapping primer sets for investigation of adjacent segments, and it is preferred to verify unexpected RT-PCR products by amplifying the same region using different primer sets.

The *TAP* splice variants described herein were first detected when attempts to isolate monoclonal antibodies recognizing either N-terminal or C-terminal epitopes of the known *TAP* subunits failed to yield C-terminal antibodies that would clear a lysate containing *TAP* subunits of all *TAP* products, whereas antibodies recognizing the N-terminus were capable of clearing solutions of all *TAP* products.

It was decided to examine *TAP1* and *TAP2* RNA samples using reverse transcription polymerase chain reaction (RT-PCR) analysis to see if plural messages were being generated. A series of forward and reverse primers were prepared for examining segments of the *TAP1* and *TAP2* coding sequences. Primers were selected to bracket relatively small segments of the genomic sequence (e.g., 300-500 bp apart), and overlapping primer sets were used (i.e., sets of primers suitable for PCR-amplifying overlapping segments of DNA).

TAP2iso cDNA was isolated from a human splenic cDNA library using an oligonucleotide probe (19 bp, SEQ ID NO: 3) complementary to exon 10 of the known *TAP2* coding sequence. The *TAP2iso* coding sequence is set forth in the Sequence Listing as SEQ ID NO: 4; the deduced amino acid sequence for *TAP2iso* is shown at SEQ ID NO: 2. The *TAP2iso* polynucleotide (SEQ ID NO: 4) encodes a polypeptide of 653 amino acids. Amino acids 1-644 are identical to a previously characterized *TAP2* (SWISS-PROT: Q03519; SEQ ID NO: 15), and the rest of the C-terminal nine amino acids are encoded by an alternatively spliced exon 12 (SEQ ID NO: 5). The novel peptide corresponding to the coding sequence of exon 12 (SEQ ID NO: 5) is referred to as the exon 12 peptide (SEQ ID NO: 1).

TAP1iso cDNA was isolated in a similar manner from a human B cell cDNA library using an oligonucleotide probe complementary to exon 8 of the known *TAP1* coding sequence. The

*TAP1iso*³ coding sequence is set forth in the Sequence Listing as SEQ ID NO: 24 (nucleotides 47-1804 of the isolated clone); the deduced amino acid sequence for *TAP1iso*³ is shown at SEQ ID NO: 25. The *TAP1iso*³ polynucleotide (SEQ ID NO: 24, nucleotides 47-1804) encodes a polypeptide of 586 amino acids. Amino acids 1-581 are identical to a previously characterized *TAP1* (SEQ ID NO: 19), and the rest of the C-terminal five amino acids are encoded by DNA 3' to the exon 8 of *TAP1* (see Fig. 11).

The polynucleotides of the present invention may be in the form of RNA or in the form of DNA, which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. The coding sequences for splice variant *TAP* isoforms according to the present invention will be partially identical and partially different (e.g., < 50 % homologous) to the known *TAP* coding sequences (i.e., *TAP1* or *TAP2*, SEQ ID NOS: 18 and 17, respectively). The *TAP2iso* coding sequence may be identical to the coding sequences shown in the Sequence Listing section (e.g., SEQ ID NO: 4) or identical to that of the deposited clone or may be a different coding sequence, which different coding sequence, as a result of the redundancy or degeneracy of the genetic code, encodes the same polypeptide. Likewise, the *TAP1iso*, *TAP1iso*², *TAP1iso*³ coding sequences may be identical to the coding sequences shown in the Sequence Listing section (e.g., SEQ ID NO: 44) or identical to those indicated in Fig. 9A or may be a different coding sequence, which different coding sequence, as a result of the redundancy or degeneracy of the genetic code, encodes the same polypeptide.

The present invention further relates to *TAPiso* transporter proteins, *TAP1iso* and *TAP2iso* splice variant proteins, and exon polypeptides. Such *TAP1* and *TAP2* splice variants will be partially identical and partially different (e.g., < 50% homologous) to the known *TAP1* and 2 subunits (i.e., SEQ ID NOS: 19 and 15, respectively); and *TAPiso* transporter proteins will be correspondingly partly identical and partly different from the known *TAP* transporter protein that consists of the heterodimer formed from *TAP1* and *TAP2*. Exon polypeptides corresponding to previously unknown exons will have coding and amino acid sequences differing substantially from any known exon of *TAP1* or *TAP2*. Specifically contemplated are *TAP2iso* proteins or exon polypeptides that have the deduced amino acid sequences of SEQ ID NOS: 1 and 2 or that have the amino acid sequence encoded by the deposited cDNA, as well as fragments thereof encoding polypeptides having the same biological function or activity as such polypeptides. The *TAPiso* polypeptides of the present invention may be recombinant polypeptides (i.e., non-naturally occurring polypeptides produced using recombinant DNA techniques), natural polypeptides or synthetic polypeptides, preferably recombinant polypeptides.

Homologues of the TAP1iso, TAP1iso², TAP1iso³, TAP1iso and TAP2iso² polypeptides described herein, as well as homologues to any subsequently discovered TAP isoforms, and homologues of exon polypeptides (i.e., peptides corresponding to the divergent sequences of such TAP isoforms), may be formed by substitution, addition or deletion of one or more amino acids
5 employing methods well known in the art and for particular purposes known in the art, such as addition of a polyhistidine "tail" in order to assist in purification or substitution of one up to several amino acids in order to obliterate an enzyme cleavage site. Preferably such homologues will retain functionality as subunits able to dimerize with counterpart TAP or TAPiso subunits in order to provide a functional TAP (or TAPiso) protein capable of translocating peptides in a cell.

10 The polypeptides and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

The present invention also provides vectors that include *TAPiso* polynucleotides of the present invention, host cells that are genetically engineered with vectors of the invention, polypeptides produced by culturing such genetically engineered host cells. Host cells are genetically
15 engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the *TAPiso* genes. The culture conditions, such as temperature, pH and
20 the like, are those suitable for use with the host cell selected for expression and will be apparent to the skilled practitioner in this field.

The polynucleotides of the present invention may be employed for producing polypeptides by recombinant DNA techniques or, preferably, for transfecting cells to augment their capability to translocate cytosolic peptides to the ER for complexing with MHC class I molecules and eventual
25 antigen display. Thus, for example, the polynucleotide may be included in any one of a variety of expression vectors for expressing a polypeptide. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. However, any other
30 vector may be used as long as it is replicable and viable in the host. The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Such procedures and others are deemed to be within the skill of those skilled in the art.

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned LTR or SV40 promoter, the *E. coli* lac or trp, the phage lambda P_L promoter and other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. In addition, expression vectors preferably will contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells, such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance for bacterial cell cultures such as *E. coli*.

The vector containing the appropriate TAP DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

As representative examples of appropriate host cells, there may be mentioned bacterial cells, such as *E. coli*, *Streptomyces*, *Salmonella typhimurium*; fungal cells, such as yeast; insect cells such as *Drosophila* and Sf9; animal cells such as CHO, COS or Bowes melanoma; plant cells, etc. However, where the object of transfection of the host cell is to form operative intracellular TAPiso proteins to augment or restore the capability of a cell to transport a particular antigen peptide or group of peptides, then mammalian cells, such as CHO or COS cells, or more particularly human cell lines, such as T cell or B cell lines, T1 or T2 cells (see *infra*), HeLa cells, U-937 cells, EBV-immortalized human B cell lines, PACA cells, and the like, are much preferred. The selection of an appropriate host is deemed to be within the skill of those skilled in the art from the teachings herein. Many suitable vectors and promoters useful in expression of proteins according to this invention are known to those of skill in the art, and many are commercially available. The following vectors are provided by way of example. Bacterial: pQE70, pQE60, pQE-9 (Qiagen), pbs, pD10, phagescript, psiX174, pbluescript SK, pbsks, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). Any other plasmid or vector may be used as long as it is replicable and viable in the selected host cell.

Introduction of the vectors into the host cell can be effected by any known method, including calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation. (see Davis et al., Basic Methods in Molecular Biology, (1986)).

The constructs in host cells can be used in a conventional manner to produce the TAP gene product encoded by the recombinant sequence. Alternatively, the polypeptides of the invention can

be synthetically produced by conventional peptide synthesis methods: For example, direct synthesis of the peptides of the invention may be accomplished using techniques including, preferably, solid-phase peptide synthesis, although solution-phase synthesis may also be used. In solid-phase synthesis, for example, the synthesis is commenced from the carboxy-terminal end of the peptide using an α -amino protected amino acid. t-Butyloxycarbonyl (Boc) protective groups can be used for all amino groups, though other protective groups are suitable. See, Stewart et al., Solid-Phase Peptide Synthesis (1989), W. H. Freeman Co., San Francisco; and Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963). Polypeptides according to the invention may also be prepared commercially by companies providing peptide synthesis as a service (e.g., BACHEM Bioscience, Inc., King of Prussia, PA; Quality Controlled Biochemicals, Inc., Hopkinton, MA). For full-length TAPiso proteins, recombinant production is most preferred, due to the practical limits and expense of protein synthesis; for smaller peptides such as exon peptides according to this invention, solid-phase synthesis or commercial synthesis will be most advantageous.

The TAP polypeptides and exon polypeptides of the present invention can be recovered and purified from recombinant cell cultures or other solutions by suitable methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin chromatography, and the like. High performance liquid chromatography (HPLC) can be employed for final purification steps. The novel polypeptides of the present invention may be a naturally purified products, or a product of chemical synthetic procedures, or produced by recombinant techniques from a prokaryotic or eukaryotic host (for example, by bacterial, yeast, higher plant, insect and mammalian cells in culture). Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated.

Functional Activity of TAP Subunit Splice Variants

TAPiso proteins according to the present invention preferably exhibit the same general functionality as known TAP transporter proteins, namely, translocation within a cell of peptides from the cytosol into the ER. However, the discoveries detailed herein demonstrate that the specific functionality of different TAP proteins, formed from different pairings of TAP1 and TAP2 isotypes, can lead to different classes of peptides being translocated, or the same peptide being translocated preferentially or at a different rate in comparison to other peptides.

Several ways of measuring TAP protein functionality are discussed below:

A. Transport Efficiency

The rate at which different TAP isoforms transport cytosolic peptides into the ER (transport efficiency) is one way to distinguish between homologous isoforms and one basis for TAP-mediated diversity in the presentation of MHC class I antigen complexes. The transport efficiency of TAPiso proteins may be compared with that of previously characterized TAP proteins using experimental techniques such as those of the following examples.

The rate at which MHC class I antigen complexes exit the ER can be used as one measure of TAP protein transport efficiency. MHC class I does not leave the ER until and unless it complexes with an appropriate peptide. TAP transport of peptides is the sole source of cytosolic peptides in the ER. The level of a particular MHC class I antigen complex within the Golgi apparatus of a cell, therefore, is directly proportional to TAP transport of the antigen peptide into the ER.

A preferred method of measuring the rate at which MHC class I antigen complexes exit the ER is through the quantification of MHC class I proteins of the Golgi apparatus sensitive to endoglycosidase H (endo H). Glycosylation of MHC class I proteins in the Golgi apparatus results in an increase in their molecular mass and an increase in resistance of MHC class I-linked glycans to endo H. By [³⁵S]methionine pulse-labeling of TAP-expressing or TAPiso-expressing cell cultures and chasing with unlabeled methionine at various times, the rate of MHC class I maturation in the ER can be gauged by observing differences in endo H sensitivity, e.g., compared with a TAP-deficient cell line such as T2. (See, Fig. 4A and 4B.)

B. Peptide Selectivity

Differential peptide binding specificity (peptide selectivity) is another way in which TAP isoforms may differ. All previously studied human allelic TAP polymorphs have shown no differences in peptide selectivity, however the nonallelic splice variants of the present invention have shown differences in peptide selectivity in comparison with previously studied TAP proteins.

The peptide binding domain of TAP proteins requires both a TAP1 and a TAP2 subunit. TAPiso transporter proteins including at least one TAPiso splice variant as disclosed herein, may result in the binding and translocation of a distinct class of cytosolic peptides, compared to those bound and translocated by a TAP1/TAP2 complex. This differential peptide selectivity has been demonstrated for TAP1/TAP2iso in comparison to TAP1/TAP2 (see examples, *infra*), thus the co-expression of TAP1 and TAP2 isoforms leads to diversification in peptides loaded into MHC class I molecules for antigen presentation at the cell surface.

The function of TAP proteins and the transport of different peptide repertoires can be tested by supplying known peptides, which may be labeled for ease of detection, to TAP and TAPiso

transformants and comparing their abilities to transport peptide into the ER and the rate at which transport is effected. Test peptides will preferably be of an optimal length for transport, i.e., about 6-25 amino acids in length, most preferably 8-12 amino acids in length. In a preferred assay of translocation, the test peptides are labeled with radioactive iodine (^{125}I). Additionally, glycosylation of the peptides within the ER of the MHC class I antigen complex can be monitored as an indication that successful transport and maturation of a properly formed antigen complex is taking place. One preferred method of monitoring maturation is noting increased resistance to endoglycosidase H (endo H), the principle being that as N-linked glycosylation of the MHC class I molecule proceeds to completion, the glycan structures of the protein become less susceptible to endo H cleavage.

Competitive inhibition techniques can also be used to compare translocation specificities of different TAP proteins. In such assays, two or more test peptide moieties are provided for possible transport by TAP proteins. Preferential TAP transport of a test peptide is measured by the competitive inhibition of the peptides in relation to each other. For example, one test peptide is detectably labeled (e.g., ^{125}I -labeled), and a second test peptide, labeled or unlabeled, is introduced into the cell, and the effect of the second peptide on the detectable translocation of the first test peptide is measured.

C. Restoration of Surface MHC Class I Antigen Complex Presentation

Functional TAPiso proteins of the present invention will bind and translocate peptides into the ER for MHC class I loading and eventual cell surface presentation. One preferred technique to measure the functionality of TAP1 and TAP2 isoforms, therefore, is to measure restoration of MHC class I antigen presentation in a TAP-deficient cell line, such as T2 cells (Attaya et al., *Nature*, 355:647 (1992)). A TAP-deficient cell can be transfected with *TAP1* and *TAP2* genes and/or genes encoding TAP splice variants to express a functional TAP or TAPiso transporter protein, and the extent of restoration of surface MHC class I antigen presentation on the transfected cell can then be measured.

Uses for TAP Subunit Splice Variants

The *TAPiso* genes described herein, and the TAPiso expression products and related exon polypeptides, will have many uses in the field of immunology and immunotherapy. For example, the *TAPiso* genes may be used to prepare recombinant host cells expressing only a particular TAPiso transporter protein, which cell will be useful in defining the specificity and translocation efficiency of particular TAPiso proteins. The TAPiso genes also may be used to produce useful quantities of isolated TAP1iso or TAP2iso proteins, which may be used as immunogens for the production of

monoclonal or polyclonal anti-TAP subunit antibodies or anti-exon polypeptide antibodies for use as diagnostic reagents or cell classification markers.

The *TAPiso* expression products or their fragments (including exon polypeptides), or cells expressing them, can be used as immunogens to produce antibodies recognizing such products or fragments. These antibodies can be, for example, polyclonal, monoclonal, chimeric, single-chain, Fab fragments, or the product of a Fab expression library. Various procedures are known in the art for the production of such antibodies. Antibodies generated against the polypeptide corresponding to a sequence of the present invention can be obtained by direct injection of the polypeptide into an animal or by administering the polypeptide to an animal, preferably a nonhuman animal. The antibody so obtained will then recognized or bind to the polypeptide itself. In this manner, even a sequence encoding only a fragment of a TAP1iso or TAP2iso polypeptide can be used to generate antibodies recognizing the intact native polypeptide. Such antibodies can then be used to isolate the polypeptide from tissue expressing that polypeptide or to detect expression of a particular TAP subunit or formation of a particular TAP or TAPiso transporter protein in particular cells or tissues. Moreover, a panel of anti-TAP1 or anti-TAP2 or anti-TAP heterodimer antibodies, specific to a range of TAP subunits and/or TAP heterodimers, can be used to identify and differentiate tissues and disease states corresponding to differential expression of TAP subunits or differential formation of TAP transporter proteins.

For preparation of monoclonal antibodies, any technique that provides antibodies produced by continuous cell line cultures can be used. Well known examples of such techniques include the hybridoma technique (Kohler and Milstein, Nature, 256:495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today, 4:72 (1983)), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96 (1985)).

Techniques described for the production of single-chain antibodies in U.S. Patent No. 4,946,778 can be adapted to produce single-chain antibodies recognizing immunogenic polypeptide products of this invention.

Such antibodies can be used in methods relating to the localization and activity of the *TAP* expression products described herein, e.g., for imaging these proteins, measuring levels thereof in appropriate physiological samples, and the like.

The TAPiso polynucleotides of the present invention also provide a means for screening candidate drugs to identify those capable of enhancing or inhibiting peptide transport. Such candidate drugs would be useful in upregulating or downregulating the immune response to particular antigens or for treating disorders associated with a particular ratio of TAP expression

products produced by an individual. For example, where an immune disorder is associated with higher than normal expression of a particular TAP protein or a higher than normal expression in relation to another TAP protein, then modulation of one or the other expression products to correct the expression or balance the relative expression of TAP proteins can alleviate the manifestation of the disorder. For drug candidate screening, a mammalian cell or membrane preparation expressing one or more TAP proteins can be incubated with labeled peptides in the presence of the drug candidate. The ability of drug to change the rate of translocation of the peptides by the TAP protein(s) or to block the translocation can then be measured.

The *TAPiso* polynucleotides of the present invention may also be employed in accordance with the present invention for causing expression of *TAPiso* polypeptides *in vivo*, which is often referred to as "gene therapy". For example, cells from a patient may be transfected with a polynucleotide (DNA or RNA) encoding a TAP polypeptide *ex vivo*, using known transfection techniques. The resultant transfectants expressing the introduced polynucleotide can reverse a TAP deficiency in the host cell, or supplement low expression of a particular subunit by the host cell, or provide an additional TAP transporter protein in the cell, thus augmenting the repertoire of MHC class I antigen complexes that are displayed by the host cell. The transfectants then can be provided to a patient to be treated. Such gene therapy methods are well known in the art.

Similarly, cells may be engineered *in vivo* for expression of a TAP polypeptide *in vivo* by procedures known in the art. For instance, a cell producing a retroviral particle containing RNA encoding the TAP polypeptide of interest may be administered to a patient for infection and transformation of the patient's cells *in vivo* and expression of the particular TAP polypeptide *in vivo*. Alternatively, known microinjection techniques can be employed to insert plasmid DNA into cells of a patient, thereby augmenting the class I antigen display of those cells and prompting a desired immune response. These and other methods for administering the polynucleotides or using a polypeptide of the present invention will be apparent to those skilled in the art from the foregoing description and the examples to follow.

In addition to gene therapy, the TAP splice variants disclosed herein may be used in improving vaccine designs or in overcoming weak immune responses in an individual to a pathogen. For example, there may be viruses that are able to avoid immune detection and attack in certain individuals because of inadequate transport of viral antigen peptides into the ER for complexing with MHC class I molecules and ultimate presentation on the cell surface. Such viruses expose a "hole" in the immune system, i.e., a gap in the antigen presentation repertoire that leads to an inability of the immune system to recognize and respond to the viral antigens, even though there are T cells bearing receptors expressed by the individual capable of binding the antigens if properly

presented. Where such inadequate transport of viral antigen peptides is the result of low expression or no expression of particular TAP variants, the *TAP1* and *TAP2* genes disclosed herein can be used to broaden the immune responsiveness of an individual. A preferred method for broadening an individual's immune responsiveness is by *ex vivo* transfection of MHC class I expressing cells, preferably lymphocytes, most preferably B cells, macrophages or dendritic cells, with DNA encoding TAP isoforms that are not expressed or are expressed at low levels, followed by reintroduction of the transfected cells into the individual, where the expression of additional TAP isoforms leads to presentation of additional antigen peptides, which, in turn, drives selection and proliferation of responsive T cells. The DNA encoding the non-expressed or inadequately expressed TAP isoform used in transfection may be specific or non-specific for the antigens derived from a particular pathogen, that is, the range of antigen peptides and thus the repertoire of displayed antigen complexes will be broadened by transfecting DNA encoding any supplementary isoform of TAP, but alternatively, if it is determined what antigen peptides result from proteolysis of a particular virus and if it is determined that the function of a particular TAP isoform leads to the translocation of such antigen peptides, then the transfection using the appropriate TAP isoform-encoding DNA will tailor the broadened immune response to the particular virus by causing an increase in the MHC class I/viral antigen complexes being presented by transfected cells. The effect of this vaccination will also continue past the cell *in vivo* life of the transfectants, because transient presentation of the supplemental repertoire of viral antigens will establish a T cell memory, and the individual challenged subsequently by the same virus will be able to mount a classic secondary antigen response.

This approach can also be used to address infectious diseases, especially where an individual's susceptibility to a disease is due to inadequate expression of a particular TAP isoform. In this way an individual can also be vaccinated to fight malignancies that escape immune attack due to inadequate presentation of antigen peptides associated with the malignant tissues. This approach would be especially useful in cases where a family history revealed a predisposition for developing certain cancers, such as breast cancer. If individuals from that family also showed abnormal expression of any of the TAP isoforms, transfected cell therapy could be used to correct the TAP deficiency or to balance the levels of expression of TAP isoforms to reflect normal levels.

Isolation, testing and use of particular TAP splice variants of the present invention will be further illustrated in the following examples. The specific parameters included in the following examples are intended to illustrate the practice of the invention, and they are not presented to in any way limit the scope of the invention.

EXAMPLE 1: TAP2iso

Described below is the isolation and characterization of a novel TAP2 splice variant (i.e., TAP2iso) that, when complexed with TAP1, forms a novel TAP heterodimer (TAP1/TAP2iso) distinct from the known TAP transporter protein. TAP2iso lacks TAP2 exon 11 and contains a newly-identified TAP2 exon 12, located 6533 base pairs (bp) downstream of TAP2 exon 11 (see Fig. 1). The 2496 bp full-length cDNA of TAP2iso (see SEQ ID NO: 4) predicts a protein of 653 amino acids (SEQ ID NO: 2), the last nine of which are encoded by exon 12 (Figs. 2 and 3). The protein encoded by this cDNA shows the ability to dimerize with TAP1 and to form a peptide-transporting heterodimer, however that TAP1/TAP2iso transporter exhibits characteristics that differ from those of the previously identified TAP.

Isolation of TAP2iso

The existence of heterofunctional TAP1 and 2 isoforms was detected during the course of work to isolate antibodies to the C-terminus of each of the known TAP subunits, TAP1 and TAP2. Whereas polyclonal antibodies recognizing epitopes of the N-terminal sequences of TAP1 and TAP2 had been isolated which would clear a cell lysate of all TAP expression products, polyclonal antibodies raised against the known C-terminal sequences were unable to remove all TAP proteins from a solution. One explanation of this phenomenon was that there were variant isoforms of the known TAP subunits differing at the C-terminal end to a sufficient degree that they could not be recognized by antibodies raised against only the known C-terminal sequences. Since a polyclonal antiserum would be expected to clear all of the known polymorphs of TAP1 and TAP2, it was decided to search for TAP1 and 2 splice variants exhibiting entirely heterologous C-terminal sequences compared to the known TAP1 and 2 proteins.

It was decided to examine a cDNA library with probes complementary to a sequence coding for an upstream segment of the TAP1 and TAP2 proteins, to see if variant transcripts could be detected. Probes were designed using sequence information of the entire locus including the known TAP genes, generously provided by Dr. John Trowsdale and colleagues at the Imperial Cancer Research Fund, London (GB). When a specific 19-base pair (bp) oligonucleotide probe complementary to exon 10 of TAP2 was used to screen a human spleen cDNA library prepared from a single individual, two different full-length transcripts were detected and analyzed.

The human splenic cDNA library was screened with the use of a soluble hybridization system (Gene Trapper; Life Technologies, Inc., Gaithersburg, Maryland (US)). The specific oligonucleotide probe (5'-ATGTAGGGGAGAAGGGAAG-3', identified as SEQ ID NO: 3) targeted to exon 10 of TAP2 was synthesized and purified by electrophoresis on a 12% polyacrylamide gel

[acrylamide: bisacrylamide, 19:1 (w/w)] containing 8 M urea with 1X Tris-borate-EDTA buffer. The probe (3 μ g) was biotinylated with the use of terminal deoxynucleotidyl transferase and biotin-conjugated deoxycytidine triphosphate. The cDNA library was digested for 25 minutes at 25°C with Gene II (Gibco-BRL), an enzyme that introduces random nicks into DNA, and then for 60 minutes at 37°C with *Escherichia coli* exonuclease III to generate single-stranded plasmid DNA. Hybridization between single-stranded plasmid DNA and 20 ng of the biotinylated probe was performed in solution for 60 minutes at 37°C. The mixture was then incubated for an additional 20 minutes with streptavidin-coated magnetic beads, after which the beads were separated and the hybridization complexes eluted.

The single-stranded cDNA was converted to double-stranded DNA by incubation for 15 minutes at 70°C in a final volume of 30 μ l containing 2U of Taq polymerase, 20 ng of non-biotinylated probe as primer, and 200 nM of each deoxynucleoside triphosphate. The double-stranded DNA was inserted into a cloning vector (PREP 8, Invitrogen) having an ampicillin resistance marker, and *Escherichia coli* were transformed with 3 μ l of the resulting DNA by electroporation at 1800 V, 25 μ F, and 100 ohms. The bacteria were plated onto four agar plates containing ampicillin (100 μ g/ml). Positive colonies were sequenced by primer walking.

The sequence of one full-length *TAP2* clone, 0123, was identical in the 5' untranslated region and in exons 1 through 10 to that of previously characterized *TAP2* cDNAs as well as to that of other *TAP2* clones (such as clone 0121) isolated from the same library. However, clone 0123 lacked exon 11 and the 3' untranslated region of the other known *TAP2* cDNAs and contained a new 27 bp exon (exon 12) and 3' untranslated region. The exon 12 sequence is present in the *TAP2* genomic sequence 6533 bp downstream of exon 11. Sequencing of the predicted splice sites confirmed the presence of functional motifs to allow the splicing of exon 10 to exon 11 (clone 0121) and exon 10 to exon 12 (clone 0123). Of the 26 informative cDNAs isolated using the exon 10 probe (SEQ ID NO: 3), 9 corresponded to the new splice form, which was designated *TAP2iso*.

The predicted *TAP2iso* protein encoded by *TAP2iso* contains 653 amino acids, compared with 703 amino acids for the previously characterized *TAP2*; the COOH-terminal nine residues of *TAP2iso* are encoded by exon 12. Alignment of amino acid sequence, hydrophobicity and secondary structure were analyzed by GCG program-SEG, MAP, TRANSLATION and PEPLOT (Genetics Computer Group, Madison, WI). Hydrophobicity analysis revealed a higher β factor for *TAP2iso* and in contrast a greater α factor for *TAP2*.

Vector Construction and Transfection

The *TAP1* (*TAP1 A* allele) cDNA was removed from the pCMV-SPORT vector (Gibco-BRL) by *Bam*HI and *Sal*II digestion and inserted into the PREP 4 vector (Invitrogen) at the *Bam*HI and *Xho*I sites. *TAP2* (clone 0121, *TAP2 F* allele) and *TAP2iso* were removed from pCMV-SPORT vector by digestion with *Not*I and *Kpn*I and inserted into the PREP 8 vector (Invitrogen) at the *Not*I and *Kpn*I sites.

Plasmid DNAs were prepared using MAXI-PREP kits (Qiagen). *TAP1*- and *TAP2*-deficient T2 cells (donated by P. Cresswell, Howard Hughes Medical Institute, Yale University) ($1-2 \times 10^7$ cells/ml) were transfected by electroporation with 10 μ g of *TAP1* and *TAP2* or *TAP2iso* linear plasmid DNA in a 0.4-cm cuvette at 260 V and 960 μ F. Subcloning and selection of transfectants were performed by culturing in the presence of hygromycin (250 μ g/ml) or histidinol (2 mM) for the PREP 4 and PREP 8 vectors, respectively.

Stable transfectant clones were analyzed by indirect immunofluorescence as described in Fu et al., *J. Clin. Invest.*, 91:2301 (1993), with an anti-HLA class I (A2) murine monoclonal antibody (clone 0791HA; One Lambda, San Diego, California (US)) and an anti-HLA class II murine monoclonal antibody (clone L243, ATCC accession no. HB55, Manassas, Virginia (US)). Immune complexes were detected with fluorescein isothiocyanate-conjugated goat anti-mouse IgG antibodies (Coulter, Hialeah, Florida (US)) and an Epics Elite flow cytometer (Coulter).

Transport Efficiency of *TAP2iso* in the Transport of Peptides to the ER

The rate at which MHC class I antigen complexes exit the ER was measured in T2 cells stably transfected with *TAP1* and either *TAP2* or *TAP2iso*, as a measure of *TAP1/TAP2iso* transport efficiency in comparison to *TAP1/TAP2*. T2 cells were transfected with *TAP1* and *TAP2iso* cDNAs, harvested at 4°C and cultured for 30 minutes in methionine-free medium. High density cells (1×10^8 cells/ml) were labeled for 15 minutes in the presence of 500 μ Ci [35 S]methionine (Amersham), and then chased at the indicated times in the presence of 10 mM unlabeled methionine.

Cells were lysed in an ice-cold lysis buffer, and lysates were incubated overnight at 4°C with protein A Sepharose beads (Pharmacia) and normal rabbit serum (1:200 dilution). The beads were removed by centrifugation and the resulting supernatant was incubated for 12 hours at 4°C with protein A beads and monoclonal antibody W6/32 (American Type Culture Collection (ATCC) accession no. HB 95, Manassas, Virginia (US)), which recognizes HLA class I molecules. The beads were separated by centrifugation and washed extensively, after which proteins were eluted from the beads by boiling for 5 minutes in SDS sample buffer and analyzed by 12.5% of SDS

polyacrylamide gel electrophoresis. The gel was treated with enhancer, dried, and exposed to X-ray film for 12 to 72 hours.

The results are shown in Figures 4A and 4B. Samples were incubated in the absence (-) or presence (+) of endo H as described in Neefjes et al., Eur. J. Immunol., 25:1133 (1995). "r" and "s" indicate HLA class I proteins resistant and sensitive to endo H, respectively. The results revealed that TAP2iso (Fig. 4A) and TAP2 (data not shown) both expressed with TAP1 showed increasing HLA class I maturation as reflected in decreasing endo H sensitivity to similar extents relative to that apparent in untransfected T2 cells (Fig. 4B).

10 Peptide Selectivity of TAP2iso in the Transport of Peptides to the ER

The peptide selectivities of TAP1/TAP2 and TAP1/TAP2iso heterodimers were compared by measuring the transport of ¹²⁵I-labeled peptides into the ER of transfected T2 cells permeabilized with streptolysin O. Peptides that have entered the ER were detected on the basis of their consequent glycosylation.

The transport of three different peptides was measured: Test Peptide RRYQNSTEL (SEQ ID NO: 6), which is a variant of a peptide eluted from HLA class I B27 (Androlewicz et al., Proc. Natl. Acad. Sci. U.S.A., 91:12716 (1994)), with a polar asparagine substituted for a charged lysine at position 5 to produce an NXT motif for glycosylation; Test Peptide IYLGPFSNVTL (SEQ ID NO: 7); and Test Peptide TVDNKTRYE (SEQ ID NO: 8), which is transported efficiently by the product of the rat *TAP2^a* allele but poorly by that of the rat *TAP2^b* allele (Momburg et al., Nature, 367:648 (1994); Fu et al., J. Clin. Invest., 91:2301 (1993); Ortmann et al., Nature, 368:864 (1994)). The size of all test peptides fell within the range of 8-12 amino acids that is optimal for transport by all TAP proteins characterized to date.

The test peptides were synthesized by Quality Controlled Biochemical, Inc. (Hopkington, MA), and their sequences were confirmed by mass spectrometry. The purity of peptide preparations was >95% as judged by high-performance liquid chromatography. 10 mM stock solutions of peptides were prepared in dimethyl sulfoxide. Peptides (25 µg) were directly iodinated at unique tyrosine residues with the use of chloramine T (Sigma, St. Louis, MO), and free iodine was removed by gel filtration using Sephadex G10 (Pharmacia) column chromatography. The specific activity of the ¹²⁵I-iodinated peptides ranged from 20 to 50 cpm/fmol.

Glycosylated ¹²⁵I-labeled Peptide RRYQNSTEL (SEQ ID NO: 6), Peptide IYLGPFSNVTL (SEQ ID NO: 7), or Peptide TVDNKTRYE (SEQ ID NO: 8) was recovered and measured. The peptide translocation assay was performed essentially as described by Neefjes et al., in Science, 261:769 (1993) and Momburg et al., in J. Exp. Med., 179:1613 (1994). Briefly, $2.5-5.0 \times 10^6$ T2

cells (transfected or untransfected) were washed once with incubation buffer (130 mM KCl, 10 mM NaCl, 1 mM CaCl₂, 2 mM EDTA, 2 mM MgCl₂, 5 mM Hepes, pH 7.3) and permeabilized for 10 minutes at 37°C with streptolysin O (2 IU/ml) (Wellcome, Beckenham, UK) in 50 µl of incubation buffer. After further addition of 10 µl of 100 mM adenosine triphosphate, 10 µl of ¹²⁵I-labeled peptide (~15 pM), and 30 µl of incubation buffer, cells were incubated for an additional 10 minutes at 37°C. Transport was terminated by the addition of 1 ml of 1% NP-40 detergent, after which nuclei were removed by centrifugation and glycosylated peptides were recovered using concanavalin A-Sepharose (Sigma, St. Louis, Missouri (US)) and quantitated with a gamma counter (LKB-Wallac).

The results are shown in Figure 5 as means ± SD of 3 independent experiments with 10 different clones. Peptide RRYQNSTEL was transported to similar extents by TAP1/TAP2 and TAP1/TAP2iso, while Peptide TVDNKTRYE was transported to a greater extent by TAP1/TAP2 than by TAP1/TAP2iso, and Peptide IYLGPFSPNVTL was transported to a greater extent by TAP1/TAP2iso than by TAP1/TAP2. The amount of translocated peptide is shown as the percentage of the input radioactive peptide. Untransfected T2 cells or those expressing TAP1 or TAP2iso alone did not show appreciable transport of any test peptide.

Differential peptide selectivity of the TAP1/TAP2 and TAP1/TAP2iso heterodimers was further investigated by competition experiments with ¹²⁵I-labeled Peptide RRYQNSTEL (SEQ ID NO: 6) and various unlabeled peptides: Peptide RRYQNSTEL (SEQ ID NO: 6); Peptide IYLGPFSPNVTL (SEQ ID NO: 7); Peptide TVDNKTRYE (SEQ ID NO: 8); Peptide SYSMEHGRWGKPVGKKRRPVKVYP (SEQ ID NO: 9), the S1-24 fragment of human adrenocorticotrophic hormone); and Peptide RGFFYTPKA (SEQ ID NO: 10), residues 22 to 30 (human insulin B chain). The iodinated 9-mer Peptide RRYQNSTEL was translocated in the presence of different concentrations of unlabeled competition peptides. The glycosylated peptides were recovered by Con A-Sepharose and quantitated. Figures 6A-6E graphically illustrate the results of: (6A) competition of ¹²⁵I-Peptide RRYQNSTEL with unlabeled Peptide RRYQNSTEL (self); (6B) competition of ¹²⁵I-Peptide RRYQNSTEL with Peptide IYLGPFSPNVTL; (6C) competition of ¹²⁵I-Peptide RRYQNSTEL with Peptide TVDNKTRYE; and (6D) competition of ¹²⁵I-Peptide RRYQNSTEL with Peptide SYSMEHGRWGKPVGKKRRPVKVYP; and (6E) competition of ¹²⁵I-Peptide RRYQNSTEL with Peptide RGFFYTPKA.

Unlabeled Peptide RRYQNSTEL inhibited transport of ¹²⁵I-labeled Peptide RRYQNSTEL in TAP1/TAP2 and TAP1-TAP2iso transfectants to similar extents; the median inhibitory concentration (IC₅₀) was ~0.15 µM in both instances (Fig. 6A). With unlabeled Peptide IYLGPFSPNVTL as competitor, transport of ¹²⁵I-Peptide RRYQNSTEL was inhibited to a markedly

greater extent in TAP1/TAP2iso transfectants than in TAP1/TAP2 transfected cells (Fig. 6B). With unlabeled Peptide TVDNKTRYE as competitor, transport of ¹²⁵I-Peptide RRYQNSTEL was inhibited to a markedly greater extent in TAP1/TAP2 transfectants than in TAP1/TAP2iso transfectants (Fig. 6C). Peptide SYSMEHGRWGKPVGKKRRPVKVYP, a 24-residue peptide, did not inhibit transport of Peptide RRYQNSTEL in either transfectant to a substantial extent (Fig. 6D), which is consistent with previous studies of TAP transporters showing a preference for peptides of 8 to 12 amino acids. Finally, Peptide RGFFYTPKA inhibited the transport of Peptide RRYQNSTEL in TAP1/TAP2iso to a greater extent than that mediated by TAP1/TAP2 (IC₅₀ values of 0.11 and 0.3 μM, respectively) (Fig. 6E). Thus, the two transporter heterodimers showed opposite preferences with regard to three of the five test peptides.

TAP2iso Restoration of MHC Class I Antigen Complex Surface Presentation in T2 Cells

The introduction of *TAP1* and *TAP2* genes into mutant T2 cells has been shown to restore the normal processing and surface expression of HLA class I molecules (Attaya et al., *Nature*, 355:647 (1992); Spies and DeMars, *Nature*, 351:323 (1991); and Powis et al., *J. Exp. Med.*, 173:913 (1991)). Here, the functional properties of TAP2 and TAP2iso were compared by testing the effects of TAP2- or TAP2iso-containing TAP heterodimers on surface HLA class I antigen complex expression.

T2 cells were transfected with *TAP1* cDNA in combination with *TAP2* or *TAP2iso* cDNAs as described above. The surface expression of MHC class I molecule A2 and the and MHC class II epitope recognized by monoclonal antibodies 0791HA and L243, respectively, were examined by flow cytometry in T1 cells or T2 cells transfected with TAP1 and either *TAP2* or *TAP2iso* cDNAs.

Flow cytometric analysis revealed that transfection of T2 cells with *TAP1* or *TAP2iso* cDNAs alone had no effect on surface expression of HLA class I (see Table 1, below). In contrast, transfection of T2 cells with *TAP1* and *TAP2* or *TAP1* and *TAP2iso* cDNA combinations resulted in restored surface expression of MHC class I. Surface MHC class I expression was ~30% greater in cells transfected with *TAP1* and *TAP2iso* cDNAs than in those transfected with *TAP1* and *TAP2* cDNAs. Consistent with the fact that T2 cells have a large homozygous deletion that encompasses both *TAP* and MHC II genes, only parental T1 cells were stained with antibodies to human MHC class II (Fig. 7).

Table 1. Restoration of surface expression of HLA class I (A2) on T2 cells transfected with both *TAP1* and either *TAP2* or *TAP2iso* cDNAs.

Cell Line	mRNA			Mean fluorescence of HLA class I (A2)* Mean \pm SD
	<i>TAP1</i>	<i>TAP2</i>	<i>TAP2iso</i>	
T1	(+)	(+)	(+)	8.43 \pm .21
T2				5.26 \pm .20
T2 (TAP1/2iso)	(+)		(+)	11.16 \pm .50 [†]
T2 (TAP1/2)	(+)	(+)		7.59 \pm .31
T2 (TAP2)			(+)	6.11 \pm 1.09
T2 (TAP1)	(+)			5.19 \pm .35

*Data are means \pm SD for four separate experiments performed over a 6-month period with at least three stable clones for each transfection group. [†]P<0.001 vs. T2 cells transfected with *TAP1* and *TAP2* cDNAs.

TAP2iso Expression in Various Human Cell Lines

Reverse transcription polymerase chain reaction (RT-PCR) analysis and sequencing of the RT-PCR products was conducted to determine the presence of TAP2iso expression in various human cell lines.

RT-PCR was performed with total RNA prepared from the various cell lines with Trizol reagent (Gibco-BRL). For the *TAP2* and *TAP2iso* cDNAs, PCR was performed with a shared primer targeted to exon 10 (SEQ ID NO: 3) and two different antisense primers targeted to the 3' untranslated region following exon 11 (SEQ ID NO: 11) and the 3' untranslated region following exon 12 (SEQ ID NO: 12), respectively. β_2 -microglobulin RNA was amplified for a RT-PCR control, and the primers used are shown at SEQ ID NO: 13 and SEQ ID NO: 14.

First strand cDNA was synthesized from 3 μ g of RNA by incubation at 42°C for 50 minutes in a final volume of 50 μ l containing 200 U of Superscript II reverse transcriptase (Gibco-BRL), 0.05 μ g of oligo(dT), and 200 nM of each deoxynucleoside triphosphate. A portion (1.5 to 3.0 μ l) of the reaction mixture was then subjected to PCR in a final volume of 50 μ l containing 0.1 nM of each primer, 200 nM of each deoxynucleoside triphosphate, and 2.5 U of Taq polymerase. After an initial denaturation step of 94°C for 2 minutes, amplification was performed for 36 cycles of 94°C for 30 sec., 57°C for 30 sec. and 72°C for 1 min. PCR products were analyzed by agarose gel electrophoresis and sequenced using DNA polymerase (Sequenase 2.0, Amersham Life Science, Arlington Heights, Illinois (US)).

Results are shown in Fig. 3. RT-PCR analysis revealed the presence of both *TAP2* and *TAP2iso* mRNAs in human fresh peripheral blood lymphocytes (lanes 3 and 4), Epstein-Barr virus-immortalized B cell lines (lanes 5 and 6), MOLT-4 acute lymphoblastic leukemia cells (lane 7), THP-1 monocytic cells (lane 8), U-937 histocytic lymphoma cells (lane 9), HeLa epithelioid carcinoma cells (lane 10), and PACA pancreatic carcinoma cells (lane 11). The presence of *TAP2* and *TAP2iso* mRNAs in T1 cells, a human lymphoblastoid B cell line (lane 1), but not in T1-derived T2 cells (lane 2), which contain a large homozygous deletion of the HLA class II region that encompasses the *TAP1* and *TAP2* genes, confirmed the specificity of the RT-PCR and was also consistent with *TAP2iso* mRNA being a splice product of *TAP2* rather than being derived from a distinct gene located elsewhere in the genome.

EXAMPLE 2: Detection of *TAP1iso* and *TAP1iso*²

Multiple samples of cDNA were analyzed using PCR primers designed using genomic sequence information of the DNA linking the coding regions of the 3' exons known for *TAP1* DNA, i.e., exons 9, 10 and 11 (and the introns). Two PCR primers were designed: The forward primer (from exon 9) was: 5'-TAGTTTCATCTCTGGACTCCCTCA-3' (SEQ ID NO: 20); the reverse primer (from the intron following exon 10) was: 5'-AGGTGTCTTTGCCTCGTCTTCT-3' (SEQ ID NO: 21). Total RNA, mRNA and cDNA samples were prepared from various cell lines. First strand cDNAs were synthesized from 3 µg of RNA or 0.5 µg of mRNA by incubating at 42°C for 50 min. in a final volume of 50 µl. A portion of the reaction mixture was then subjected to PCR with the above set of primers. PCR products were then analyzed by agarose gel electrophoresis, and some samples were recovered for DNA sequencing. Analysis of the PCR products revealed the presence of two unexpected PCR products not corresponding to the expected *TAP1* product but present in all human cell samples tested. This indicated two additional splice variants corresponding to *TAP1*, and these were designated *TAP1iso* and *TAP1iso*². The fact that the two variants appeared in all samples indicated that the variants were not allelic polymorphs but were variants of the original gene.

Referring to Fig. 8, results of electrophoresis of the RT-PCR products from various samples using the above primers are shown. Lane 1 shows molecular weight markers; lane 2 shows PCR products from genomic DNA of and EBV-immortalized B cell line from a first individual (Control #1); lane 3 shows RT-PCR products from nuclear mRNA from the same Control #1 cell line; lane 4 shows RT-PCR products from cytoplasmic mRNA from Control #1; lane 5 shows RT-PCR products from total RNA from Control #1, without DNAase; lane 6 shows RT-PCR products from total RNA from Control #1, with DNAase digestion; lane 7 shows RT-PCR products from cytoplasmic mRNA

of an EBV-immortalized B cell line from a second individual (Control #2), with DNAase digestion; lane 8 shows RT-PCR products from cytoplasmic mRNA of an EBV-immortalized B cell line from a third individual (Control #3), with DNAase digestion; lane 9 shows RT-PCR products from cytoplasmic mRNA of an EBV-immortalized B cell line from a fourth individual (Control #4), with DNAase digestion; and lane 10 shows RT-PCR products from cytoplasmic mRNA of an EBV-immortalized B cell line from a patient with type I diabetes.

As can be seen in the figure, the high molecular weight PCR product amplifying the entire sequence spanning the intron between exons 9 and 10 is clearly visible in samples including genomic DNA or unspliced RNA (lanes 2, 3 and 5). Cytoplasmic and nuclear mRNA are compared (e.g., lanes 3 and 4) to confirm that the unexpected products are not amplified mRNA that has not been completely spliced. Comparison of cytoplasmic mRNA from several individuals (e.g., lanes 4 and 6-10) confirms that the TAP1iso and TAP1iso² products are splice variants and not random mutations. The relative intensities of the signals is intriguing, in that it suggests that expression ratios may differ to some extent from individual to individual, and the equal, intense bands shown in the diabetic subject (lane 10) suggest a possible link between TAP1 isoform expression and the disease (see, also, Example 4, *infra*).

Sequencing of the TAP1iso and TAP1iso² bands showed that TAP1iso represented a splice form containing exon 9, exon 10 and retaining intron 10 at least to the primer location, and that TAP1iso² contained both exons 9 and 10 but a smaller portion of retained intron 10. A comparison of the PCR products is shown in Fig. 9A. A schematic diagram of the relationship between genomic DNA and the DNA indicated by the PCR products is shown in Fig. 9B. The heavy-lined area of intron 10 indicates the section of the intron common to both splice variant PCR products, up to the primer boundary.

EXAMPLE 3: Detection of TAP2iso²

Using methods similar to those described above, cDNA derived from cytoplasmic mRNA of PBLs from multiple human donors was amplified and analyzed by gel electrophoresis to determine whether additional TAP2 splice variants could be detected using two exonic primers. The forward primer was: 5'-GCTACTAGTGCCCTAGATGTGCAGT-3' (SEQ ID NO: 22), located in TAP2 exon 10; and the reverse primer was: 5'-CTTCTGCAGCTTGCCCTCCTGGAG-3' (SEQ ID NO: 23), located in TAP2 exon 11.

Analysis of the PCR products showed that PBLs of all of the donors exhibited the fully spliced TAP2 message (lower arrow, Fig. 10) but that some donors also exhibited a larger product (middle arrow, Fig. 10) with presumed partial retention of intron 10 sequence. This second product

indicated a second TAP2 splice variant, which included at least portions of exons 10 and 11 and a portion of intron 10. This splice variant was designated TAP2iso². The control genomic DNA sample (lane 11, upper arrow) showed an expected very large molecular weight PCR product including amplified DNA that is present in neither of the TAP2 splice variants. Referring to Fig. 10, lane 1 shows the PCR products derived from cytoplasmic mRNA from a first individual; lane 2 shows the PCR products derived from cytoplasmic mRNA from a second individual; lane 3 shows the PCR products derived from cytoplasmic mRNA from a hypothyroid patient; lane 4 shows the PCR products derived from cytoplasmic mRNA from a third individual; lane 5 shows the PCR products derived from cytoplasmic mRNA from a fourth individual; lane 6 shows the PCR products derived from cytoplasmic mRNA from a fifth individual; lane 7 shows the PCR products derived from cytoplasmic mRNA from a sixth individual; lane 9 shows the PCR products derived from cytoplasmic mRNA from a seventh individual; and lane 10 shows the PCR product derived from a genomic DNA sample. The bands corresponding to the TAP2iso² product are not present in three of the normal individuals (lanes 2, 6 and 9); and the hypothyroid patient does not show any readily discernable abnormality associated with the expression of these two TAP2 isoforms.

EXAMPLE 4: TAP2 Expression Ratio Association With Diabetes

A further investigation of association between TAP1 or TAP2 isotype expression and disease states was conducted by testing five patients being treated for Type I diabetes and five unaffected, non-diabetic subjects. The relative expression in each of the subjects of TAP2 and TAP2iso was determined in a RNase protection assay. All subjects were found to co-express TAP2 and TAP2iso. In four of five diabetic subjects, expression of TAP2iso greatly predominated over TAP2, where in all five non-diabetic subjects, the expression levels of TAP2 and TAP2iso were approximately even. These results and the results above indicate that some manifestations of autoimmune diseases such as diabetes may be shown to have an association with relative TAP isoform expression, and one or more aspects of TAP isoform expression may be observed to help diagnose or monitor the penetration of the disease.

Based on the discoveries herein and the links observed thus far between TAP diversity and some disease states, changes in the expression of one or more TAP isoforms will also be indicative of certain infections and malignancies that avoid immune response by interruption of specific TAP expression. Thus, differential expression of one or more TAP isoforms may also be used to diagnose and monitor infectious diseases or cancers associated with reduction, upregulation or elimination of expression of a TAP protein.

EXAMPLE 5: Isoation of TAP1iso³

Using the same techniques as described in Example 1, supra, a further TAP1 isoform cDNA (designated TAP1iso³) was isolated, using a probe targeted to TAP1 exon 8 and a cDNA library made from B lymphocytes obtained from a normal individual. The library was probed using the same solution hybridization technique.

The sequence of a full-length TAP1 splice variant clone (SEQ ID NO: 24) was isolated which was identical in the 5' untranslated region and in exons 1 through 8 to that of previously characterized TAP1 cDNAs. However, the new TAP1 cDNA clone lacked exons 9, 10 and 11 and the 3' untranslated region of the other known TAP1 cDNAs, and it contained coding sequence for an additional five amino acid residues in frame with the 3' end of exon 8, and a new 3' untranslated region. A schematic diagram of the genomic DNA including TAP1 exons 1-11, with diagrams of the TAP1 and TAP1iso³ messages is illustrated in Fig. 11.

The predicted TAP1iso³ protein (SEQ ID NO: 25) encoded by TAP1iso³ (coding sequence = nucleotides 47-1804 of SEQ ID NO: 24) contains 586 amino acids, compared with 748 amino acids for the previously characterized TAP1 (SEQ ID NO: 19).

By following the examples given above, it is contemplated that additional splice variants of the TAP1 and TAP2 proteins will be discovered and that their specificities for different types and repertoires of antigen peptides will be mapped out. The discovery of multiple splice variants having similar but not identical transport functionality expands previous views as to the limits of antigen display by MHC class I molecules. The mechanism by which cytotoxic T cells are alerted to somatic events requiring an immune response is now seen to be more complex than originally thought, and new methods for detecting predisposition to genetically linked autoimmune disorders can now be contemplated. For example, in a disease that is characterized by a deletion or a mutation preventing expression of one or more of the TAP splice variants, gene therapy to replace expression of the lost splice variant(s), or other therapy to restore surface expression of the peptide repertoire for which the lost splice variant is specific, will effectively treat the disease. Similarly, a virus that knocks out expression of a splice variant or alters the ratio of expression of two or more splice variants, may be diagnosed by detection of the change in splice variant expression and may be combatted using vaccines designed to overcome the reduction or elimination of the MHC class I antigen complexes that results from the virus-mediated changes in splice variant expression. Some tumors may also arise through alteration of splice variant expression, and thus certain cancers may be diagnosed by detecting altered splice variant expression and treated by correcting the expression or otherwise overcoming the change in MHC class I antigen complex display that results from the

altered expression. These and other obvious applications of the discoveries herein relating to TAP splice variants are contemplated and are intended to be included in the scope of the present invention.

5

Table of Sequence Identification Numbers (SEQ ID NOS:)

SEQ ID NO:	Description
1	Amino acid sequence of TAP2iso exon 12 polypeptide
2	Amino acid sequence of TAP2iso polypeptide
3	TAP2 exon 10 oligonucleotide probe
4	Nucleic acid sequence of <i>TAP2iso</i>
5	Nucleic acid sequence of <i>TAP2iso</i> exon 12
6	Test Peptide RRYQNSTEL
7	Test Peptide IYLGPFSPNVTI
8	Test Peptide TVDNKTRYE
9	Test Peptide SYSMEHGRWGKPVGKKRRPVKVYP
10	insulin β chain ₂₂₋₃₀ : RGFFYTPKA
11	TAP2 exon 11 oligonucleotide probe
12	TAP2 exon 12 oligonucleotide probe
13	β_2 -microglobulin oligonucleotide probe
14	β_2 -microglobulin oligonucleotide probe
15	Amino acid sequence of TAP2 polypeptide
16	Amino acid sequence of TAP2 exon 11 polypeptide
17	Nucleic acid sequence of <i>TAP2</i>
18	Nucleic acid sequence of <i>TAP1</i>
19	Amino acid sequence of TAP1 polypeptide
20	Nucleic acid sequence of TAP1 exon 9 primer
21	Nucleic acid sequence of TAP1 intron 10 primer
22	Nucleic acid sequence of TAP2 exon 10 primer
23	Nucleic acid sequence of TAP2 exon 11 primer
24	Nucleic acid sequence of isolated clone including <i>TAP1iso</i> ³ coding sequence
25	Amino acid sequence of TAP1iso ³ polypeptide

All of the publications cited herein are hereby incorporated by reference in their entirety.

10

Claims

1. An isolated nucleic acid encoding a TAP1 or TAP2 splice variant.
2. An isolated nucleic acid comprising:
a polynucleotide sequence that is at least 95% identical to the sequence of a polynucleotide selected from the group consisting of
 - (a) a polynucleotide encoding a polypeptide having the amino acid sequence of SEQ ID NO: 2,
 - (b) a polynucleotide encoding a polypeptide having the amino acid sequence of SEQ ID NO: 25, and
 - (c) the complement of (a) or (b).
3. The isolated nucleic acid of Claim 2, wherein said polynucleotide (a) has the sequence of SEQ ID NO: 4.
4. The isolated nucleic acid of Claim 2, wherein said polynucleotide (a) has the sequence of SEQ ID NO: 24.
5. An isolated nucleic acid encoding a TAP2 exon 12 polypeptide.
6. The isolated nucleic acid of Claim 5, wherein said nucleic acid has the sequence of SEQ ID NO: 5.
7. An expression vector comprising the nucleic acid of Claim 1.
8. An expression vector comprising the nucleic acid of Claim 2.
9. An expression vector comprising the nucleic acid of Claim 3.
10. An expression vector comprising the nucleic acid of Claim 4.
11. An expression vector comprising the nucleic acid of Claim 5.
12. An expression vector comprising the nucleic acid of Claim 6.
13. A host cell transfected with the vector according to Claim 7.
14. A host cell transfected with the vector according to Claim 8.
15. A host cell transfected with the vector according to Claim 9.
16. A host cell transfected with the vector according to Claim 10.
17. A host cell transfected with the vector according to Claim 11.
18. A host cell transfected with the vector according to Claim 12.
19. A process for producing a polypeptide comprising culturing the host cell of Claim 13 under conditions suitable to produce the polypeptide encoded by said polynucleotide.
20. A process for producing a polypeptide comprising culturing the host cell of Claim 14 under conditions suitable to produce the polypeptide encoded by said polynucleotide.

21. A process for producing a polypeptide comprising culturing the host cell of Claim 15 under conditions suitable to produce the polypeptide encoded by said polynucleotide.
22. A process for producing a polypeptide comprising culturing the host cell of Claim 16 under conditions suitable to produce the polypeptide encoded by said polynucleotide.
23. A process for producing a polypeptide comprising culturing the host cell of Claim 17 under conditions suitable to produce the polypeptide encoded by said polynucleotide.
24. A process for producing a polypeptide comprising culturing the host cell of Claim 18 under conditions suitable to produce the polypeptide encoded by said polynucleotide.
25. A method of altering transport of peptides from the cytosol to the endoplasmic reticulum of a living cell comprising: transfecting a living cell with a vector according to Claim 7, then culturing the transfected cell under conditions suitable to produce the polypeptide encoded by said polynucleotide.
26. A method of altering transport of peptides from the cytosol to the endoplasmic reticulum of a living cell comprising: transfecting a living cell with a vector according to Claim 8, then culturing the transfected cell under conditions suitable to produce the polypeptide encoded by said polynucleotide.
27. A method of altering transport of peptides from the cytosol to the endoplasmic reticulum of a living cell comprising: transfecting a living cell with a vector according to Claim 9, then culturing the transfected cell under conditions suitable to produce the polypeptide encoded by said polynucleotide.
28. A method of altering transport of peptides from the cytosol to the endoplasmic reticulum of a living cell comprising: transfecting a living cell with a vector according to Claim 10, then culturing the transfected cell under conditions suitable to produce the polypeptide encoded by said polynucleotide.
29. A method of altering transport of peptides from the cytosol to the endoplasmic reticulum of a living cell comprising: transfecting a living cell with a vector according to Claim 11, then culturing the transfected cell under conditions suitable to produce the polypeptide encoded by said polynucleotide.
30. A method of altering transport of peptides from the cytosol to the endoplasmic reticulum of a living cell comprising: transfecting a living cell with a vector according to Claim 12, then culturing the transfected cell under conditions suitable to produce the polypeptide encoded by said polynucleotide.

31. A TAP1 splice variant having the ability to form a heterodimer in a mammalian cell with TAP2 (SEQ ID NO: 15), which heterodimer functions as a transporter associated with antigen processing protein.
32. A TAP2 splice variant having the ability to form a heterodimer in a mammalian cell with TAP1 (SEQ ID NO: 19), which heterodimer functions as a transporter associated with antigen processing protein.
33. A TAP2iso exon 12 polypeptide.
34. A TAP2iso exon 12 polypeptide having the sequence of SEQ ID NO: 1.
35. A TAP1iso³ exon 8a polypeptide.
36. A TAP1iso³ exon 8a polypeptide comprising the sequence of amino acid residues 582-586 of SEQ ID NO: 25.
37. An isolated antibody reactive with TAP1iso, TAP1iso², TAP1iso³, TAP2iso or TAP2iso² but not reactive with TAP1 (SEQ ID NO: 19) or TAP2 (SEQ ID NO: 15) or allelic variants thereof.
38. An isolated antibody according to Claim 37 reactive with TAP2iso exon 12.
39. An isolated antibody according to Claim 37 reactive with TAP1iso³ exon 8a.
40. A method for treating a disorder associated with abnormal expression of one or more TAP heterodimers comprising gene therapy to provide normal TAP heterodimer expression.
41. A method for broadening the immune response of an individual to a particular antigen comprising (a) removing lymphocytes from the individual, (b) determining whether any TAP isoform is not expressed or is inadequately expressed by the individual, (c) transfecting the lymphocytes with an isolated nucleic acid vector suitable for directing the expression by said lymphocytes of at least one of the non-expressed or inadequately expressed TAP isoforms, and (d) reintroducing the transfected lymphocytes into the individual.
42. A method for diagnosing or monitoring the course of a disease associated with abnormal or inadequate expression of a TAP isoform in an individual, comprising (a) removing a sample of MHC class I-presenting cells from the individual and (b) determining whether such cells exhibit inadequate or abnormal expression of a TAP isoform in comparison to an individual not suffering from said disease, wherein determination of such inadequate expression or abnormal expression of said TAP isoform indicates manifestation of the disease.